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Environmental Effects of Dredging Technical Notes



The Use of Population Modeling to Interpret Chronic Sublethal Sediment Bioassays

Purpose

This technical note provides a brief introduction to population modeling and describes the application and utility of such techniques for dredged material bioassays. The use of population modeling as a source of interpretive guidance for chronic sublethal dredged material bioassays is emphasized.

Background

Current laws and regulations governing the discharge of dredged material stress the importance of assessing the chronic (long-term) sublethal effects of dredging operations. Regulations implementing section 103 of the Marine Protection, Research and Sanctuaries Act (PL 92-532) state that, "Materials shall be deemed environmentally acceptable for ocean dumping only when . . . no significant undesirable effects will occur due either to chronic toxicity or to bioaccumulation . . ." Similar language is used in regulations implementing section 404(b)(1) of the Clean Water Act (PL 92-500) which reads: "The permitting authority shall determine in writing the potential short-term or long-term effects of a proposed discharge of dredged or fill material on the physical, chemical, and biological components of the aquatic environment . . ." It also stipulates that tests "may be required to provide information on the effect of the discharge material on communities or populations of organisms."

Populations and their aggregations, communities, represent the level of biological organization of greatest interest to society in general as well as to regulators (Figure 1). This interest is expressed as concern for the effects of contaminants on maintaining viable populations of commercially important species, such as oysters or striped bass, as well as other members of aquatic and marine systems. Because of the complexity inherent at the population/community level of biological organization, predicting contaminant effects at

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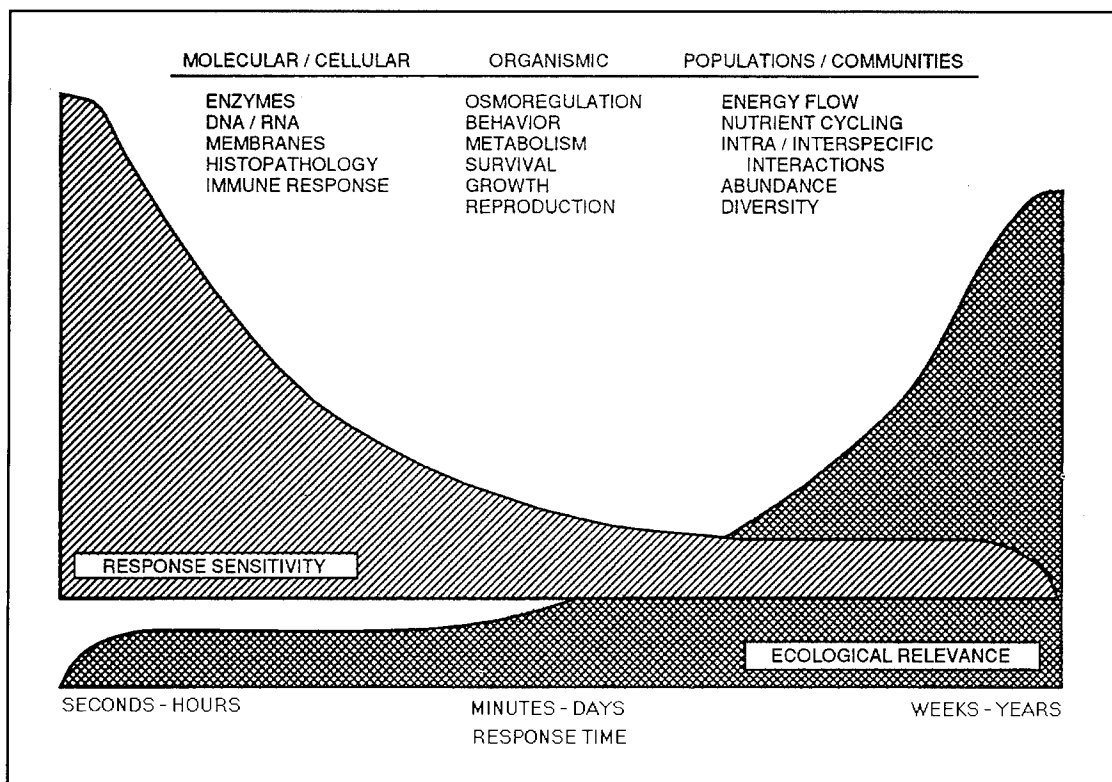


Figure 1. Levels of biological organization. Three levels of biological organization associated with chronic sublethal sediment bioassays are listed with examples of relevant level-specific processes and time scales. Bioassays at the molecular/cellular level are highly sensitive and produce results in short periods of time, but tests conducted at this level lack ecological relevance. Conversely, tests focused on populations/communities in the field have the greatest ecological relevance, but require long periods of time to perform and produce results which are difficult to interpret. Consequently, bioassays performed at the organismic level represent the optimum tradeoff between response sensitivity and ecological relevance.

this level is difficult. Consequently, the focus of dredged material testing has been on lower levels of organization where responses to contaminants are more easily recognized and understood. However, the effective use of bioassays conducted at lower levels of biological organization, that is, the molecular/cellular and organismic levels, requires the establishment of a meaningful link between results of these tests and population viability or health. How can bioassays conducted at these lower levels of organization be used to predict effects at the population/community level? Population modeling techniques provide the only mechanism for establishing this link.

Additional Information

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Interpretive Guidance for Chronic Sublethal Sediment Bioassays

A number of federal, academic, and private laboratories in the United States are currently developing chronic sublethal sediment bioassays for the evaluation of dredged material (Dillon, Gibson, and Moore 1990). Most chronic sublethal tests under development use either polychaete or amphipod species because these animals are amenable to such testing. Potential chronic sublethal test endpoints include growth, reproduction, behavior, and physiological measures of metabolic rate.

Interpretive guidance, the establishment of a link between test endpoints and ecological effects, is a necessary component of a fully developed chronic sublethal sediment bioassay (Dillon, Gibson, and Moore 1990 and Dillon 1992, 1993). The two most commonly used sublethal endpoints, growth and reproduction, provide sensitive measures of animal stress during chronic exposures to contaminated sediments (Dillon, Moore, and Gibson 1993, McGee, Schlekot, and Reinharz 1993, and Moore, Dillon, and Suedel 1991). However, the ecological meaning of growth and reproductive responses is difficult to quantify. Since current regulations are focused on protecting populations of organisms, one might ask "What would a 10 percent reduction in growth or reproduction in animals exposed to sediment during a bioassay mean for populations in the field?" Without well developed interpretive guidance, this question is impossible to answer. Population modeling represents an efficient and powerful technique for providing the necessary interpretive guidance for chronic sublethal sediment bioassays (Dillon, Gibson, and Moore 1990, Gentile and others 1982, and Pesch, Munns, and Gutjahr-Gobell 1991).

Data Requirements for Population Modeling

The construction of a population or demographic model generally requires the collection of data on survivorship, growth, and reproduction over the entire life span of the organism of concern. Chronic sublethal sediment bioassays are particularly amenable to using demographic models since these bioassays are commonly run over a major portion of the life cycle of test organisms and the endpoint data collected (survivorship, growth, and reproduction) constitute the necessary elements of a demographic model.

In laboratory settings, demographic data are collected by raising a number of individuals from birth through death under controlled conditions and collecting information on survivorship, growth, and reproduction by monitoring individuals at regular intervals (for example, daily or weekly). This procedure, though not practical for long-lived species, can be effectively applied to most species used in chronic sublethal testing since life cycles in these species are typically short (days to weeks). Two common approaches to population modeling use life table analysis and matrix population modeling.

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Life Tables and Calculation of the Intrinsic Rate of Natural Increase (r)

The dynamics and structure of populations can be described by such vital rates as birth, growth, development, and mortality (Caswell 1989). Early attempts at describing populations in these terms resulted in the development of life tables (Pearl 1928, Bodenheimer 1938, and Deevey 1947). In their simplest form, life tables contain age-specific information on survivorship (l_x) and reproduction (m_x) (Table 1). A number of parameters which describe aspects of population structure and dynamics can be calculated from l_x and m_x , including r , the intrinsic rate of natural increase. Using Euler's (1970) equation:

$$\sum_{x=0}^{\infty} e^{-rx} l_x m_x = 1 \quad (1)$$

where x is the age class, and r can be calculated using data from a life table. When the per capita birth rate (b) of a population exceeds the per capita death rate (d), r , which represents a per capita growth rate, is positive ($r = b - d$), and the population is growing. When the death rate exceeds the birth rate, r is negative, indicating that the population is declining. Such summary values as r serve to integrate age-specific information on survivorship and reproduction into a single, standard value that encapsulates the status of a population. In fact, by using the equation

$$N_t = N_0 e^{rt} \quad (2)$$

Table 1
Hypothetical Life Table Listing Age-specific Survivorship and Fecundity

Age (x)	Survivorship (l_x)	Fecundity (m_x)
0	1.0	0.0
1	0.8	0.0
2	0.7	0.2
3	0.6	0.5
4	0.4	1.0
5	0.2	0.3
6	0.0	0.0

Note: Survivorship (l_x) represents the proportion of individuals present at age 0 (newborns) that are alive at age x ; l_x can be viewed as the probability that a newborn will be alive at age x . Fecundity (m_x) represents the average number of offspring produced by an individual of age x during that age period.

population size at any time (N_t) can be calculated by knowing the population's initial size (N_0), r , and the amount of time transpired (t). However, Equation 2 will only accurately predict population size at time t (N_t) if population growth can be described in terms of an exponential growth curve (Figure 2). Other model formulations of population growth have been developed in recognition of the fact that populations in nature rarely, if ever, experience exponential growth (for example, due to limiting resources) (Pielou 1977).

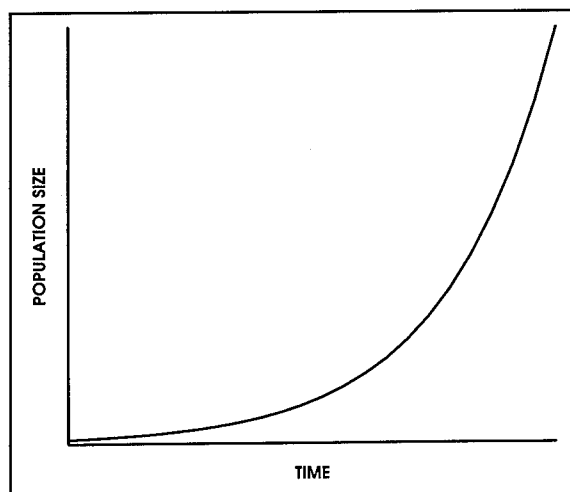


Figure 2. Exponential curve describing population growth over time using Equation 2

Matrix Population Models and Calculation of the Finite Rate of Increase (λ)

By use of matrix algebra and population projection matrices, which contain life table data in a slightly different form, matrix population models provide relatively convenient methods for deriving useful descriptive statistics for population dynamics and structure (Figure 3). Matrix population models were

$$\begin{array}{c} \mathbf{n}_{(t+1)} \\ \left[\begin{array}{c} n_1 \\ n_2 \\ n_3 \\ n_4 \\ \vdots \\ n_s \end{array} \right]_{(t+1)} \end{array} = \begin{array}{c} \mathbf{A} \\ \left[\begin{array}{cccccc} F_1 & F_2 & F_3 & F_4 & \cdots & F_s \\ P_1 & 0 & 0 & 0 & \cdots & 0 \\ 0 & P_2 & 0 & 0 & \cdots & 0 \\ 0 & 0 & P_3 & 0 & \cdots & 0 \\ \vdots & \ddots & \ddots & \ddots & \cdots & \vdots \\ 0 & 0 & 0 & \cdots & P_{s-1} & 0 \end{array} \right] \end{array} \begin{array}{c} \mathbf{n}_{(t)} \\ \left[\begin{array}{c} n_1 \\ n_2 \\ n_3 \\ n_4 \\ \vdots \\ n_s \end{array} \right]_{(t)} \end{array}$$

Figure 3. Population projection. This entire expression may be more simply expressed as $\mathbf{n}_{(t+1)} = \mathbf{A}\mathbf{n}_{(t)}$. \mathbf{A} is called a population projection matrix; in this age-classified case this matrix is also known as a Leslie matrix. The first row of \mathbf{A} contains age-specific fecundities (F_s) and the subdiagonal contains age-specific survival probabilities (P_s). The two single column matrices (or vectors) contain the number (n) of individuals in each age class at time t and one time step later ($t+1$). \mathbf{A} is referred to as a projection matrix because when it is multiplied by $\mathbf{n}_{(t)}$ the resulting vector ($\mathbf{n}_{(t+1)}$) contains the number of individuals in each age class after one time step of growth (that is, population size has been projected one time step into the future).

developed independently during the 1940s by Bernardelli (1941), Lewis (1942), and Leslie (1945), but were not in common use by ecologists prior to the 1970s (Caswell 1989).

One descriptive statistic produced by matrix population techniques is the finite rate of increase (λ), which summarizes the effect of a population projection matrix. In the case of λ , values greater than 1 mean a population is growing and values less than 1 mean a population is declining. The use of λ as a measure of population growth rate is indicated in the following equation:

$$N_t = N_0 \lambda \quad (3)$$

A population growing at a rate of $\lambda = 1.2$ /week would be increasing by 20 percent per week.

One attractive feature of matrix population models is their flexibility. This flexibility is particularly beneficial when the organism of interest has a complex life cycle where it is helpful to classify organisms according to factors other than age, for example, size or developmental stage (Caswell 1989). Complex life cycles are common among organisms used in sediment bioassays.

Using r or λ : Their Relationship and Assumptions

The life table and matrix population modeling techniques described above for producing the summary statistics r and λ actually produce equivalent results. In fact, the relationship between λ and r is related by the equations:

$$r = \log_e \lambda \quad (4)$$

or

$$\lambda = e^r \quad (5)$$

Even though the two techniques produce equivalent results, there are advantages to using matrix population models over the life table technique described. For example, the mathematics of matrix population models is more convenient than life table techniques (Caswell 1989). Other advantages of matrix population models include their flexibility as well as the fact that the meaning of λ can be more easily understood and communicated. (Equation 3 is relatively more simple than Equation 2.)

The two most important assumptions of the techniques described above involve the constancy of environmental conditions and the equilibrial status of populations. The summary statistics r and λ are based on calculations using data on survivorship and reproduction collected under a specific set of environmental conditions (usually laboratory conditions). If conditions in the field

differ from those in the laboratory in such a way that survivorship and reproduction are affected, then the summary statistics (for example, λ) may not accurately reflect population growth in the field. Additionally, the summary statistics accurately describe population growth only after the population has reached a stable age distribution; that is, the population has reached an equilibrium state in which the proportion of individuals in each age class remains constant through time. This equilibrium state is rarely if ever reached in natural populations.

Even with these limiting assumptions, population models represent a powerful way of projecting effects on populations using data collected on individual organisms. The limiting assumptions mentioned above are at least partially overcome by stochastic demographic modeling (Ferson 1991 and Burgman, Ferson, and Akcakaya 1993), a technique particularly suited for application in ecotoxicology and dredged material testing.

Application to Bioassays

Beginning with Marshall (1962), a number of studies have made use of demographic concepts and models in ecotoxicology. A variety of organisms have been used in life table response experiments (Caswell 1989) to estimate the population-level consequences of contaminants including cladocerans (Chandini 1991 and Wong and Wong 1990) and other crustaceans (Gentile and others 1982), polychaetes (Pesch, Munns, and Gutjahr-Gobell 1991), oligochaetes (Niederlehner and others 1984), nematodes (Vrannken and Heip 1986), gastrotrichs (Hummon 1974), and rotifers (Rao and Sarma 1986).

The summary statistics produced by demographic models are useful descriptors of population health or viability. For example, populations experiencing positive growth could be described as healthy, while populations with a λ less than 1 would be at risk of extinction if the environmental conditions producing the population decline persist. Such a measure of population health (λ) effectively integrates the effects contaminants have on organism survivorship, growth, and reproduction. In designing a dredged material bioassay, one might ask the question "Does population growth (λ) differ in a biologically significant way in animals exposed to dredged material compared to reference sediments?"

Answering the preceding question is the foundation of interpretive guidance for chronic sublethal bioassays. If the results of a dredged material bioassay indicate a 10 percent reduction in growth in animals exposed to dredged material compared to reference site sediment, but the λ 's for dredged material and reference exposed animals are essentially identical, one would expect the 10 percent reduction in growth to have little or no effect on population health. Used in this fashion demographic models and their summary statistics would suggest biologically reasonable criteria for judging the toxicity of sediments. If population growth is only affected when individual growth is reduced by

30 percent, then 30 percent represents a reasonable mark for judging a sediment as contaminated.

A Hypothetical Example

Figure 4 contains hypothetical results for a series of chronic sublethal sediment bioassays where data were also collected to provide interpretive guidance in the form of population growth rate (λ). The vertical axis lists the population growth rate of test animals exposed to the sediments listed on the horizontal axis. Sediment A is from a reference station, while sediments B through F are project sediments.

The population growth rate for test animals exposed to project sediment B is the same as for animals exposed to the reference sediment. Population growth rates of animals exposed to project sediments C and D were reduced in comparison to the reference sediment, but were still greater than 1. Since populations exposed to project sediments C and D were experiencing positive growth, they may be considered healthy. Population growth is further reduced in project

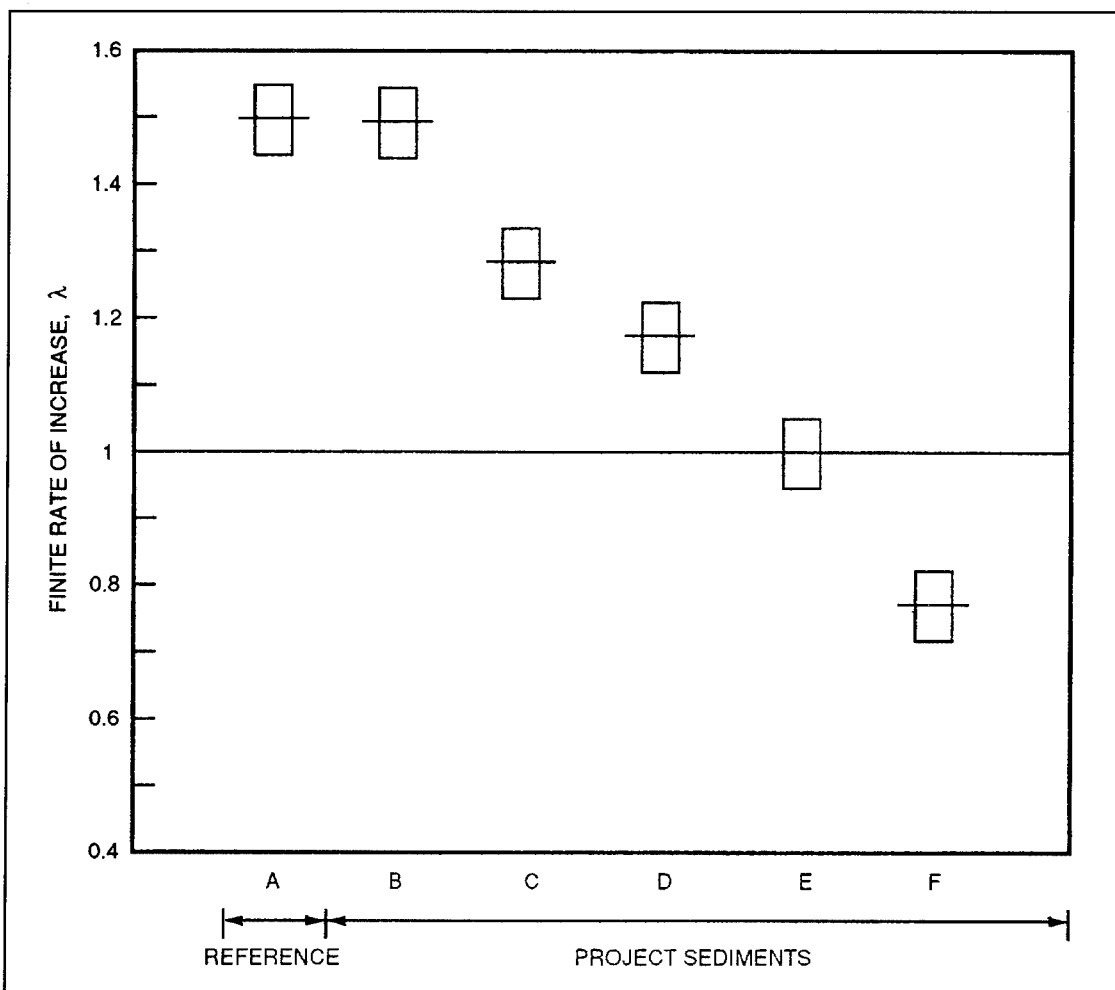


Figure 4. Results of a hypothetical series of dredged material bioassays

sediment E; in fact, λ equals 1, indicating that the population is neither growing or declining but maintaining a constant size. It would be reasonable to declare sediments resulting in a λ of less than 1 to be contaminated since a population growing at such a rate would go extinct given sufficient time (project sediment F). Used in this fashion, population modeling can provide meaningful interpretive guidance for chronic sublethal sediment bioassays.

Sensitivity Analysis

Demographic modeling techniques can even be used to design more accurate and cost-efficient chronic sublethal bioassays. Sensitivity analysis applied to matrix population models can help identify which life stages or endpoints (for example, survivorship, growth, or reproduction) are most important to population growth in the test species (Caswell 1989). If sensitivity analysis indicated that changes in survivorship of early life stages or perhaps early reproduction had the largest effect on population growth, then tests could be designed to concentrate on those endpoints. Such an approach could reduce the effort and costs incurred in performing a test while also increasing test accuracy.

Conclusions

Current laws and regulations governing the disposal of dredged material emphasize the importance of maintaining the ecological health of the environment. Current guidance for testing dredged material using sediment bioassays makes use of acute lethality tests for identifying potential threats to environmental health. Heightened awareness of the potential long-term effects of chronic low-level exposures to contaminated sediments has generated interest in the development of chronic sublethal bioassays. The major source of uncertainty in the design, performance and results of sediment bioassays concerns predicting the behavior of complex systems (for example, populations) using simple systems (for example, individual animals in a beaker). Use of demographic modeling will enhance the predictive capabilities of chronic sublethal sediment bioassays through providing an ecologically meaningful way of interpreting results and designing future bioassays.

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